65/81

Figure 97

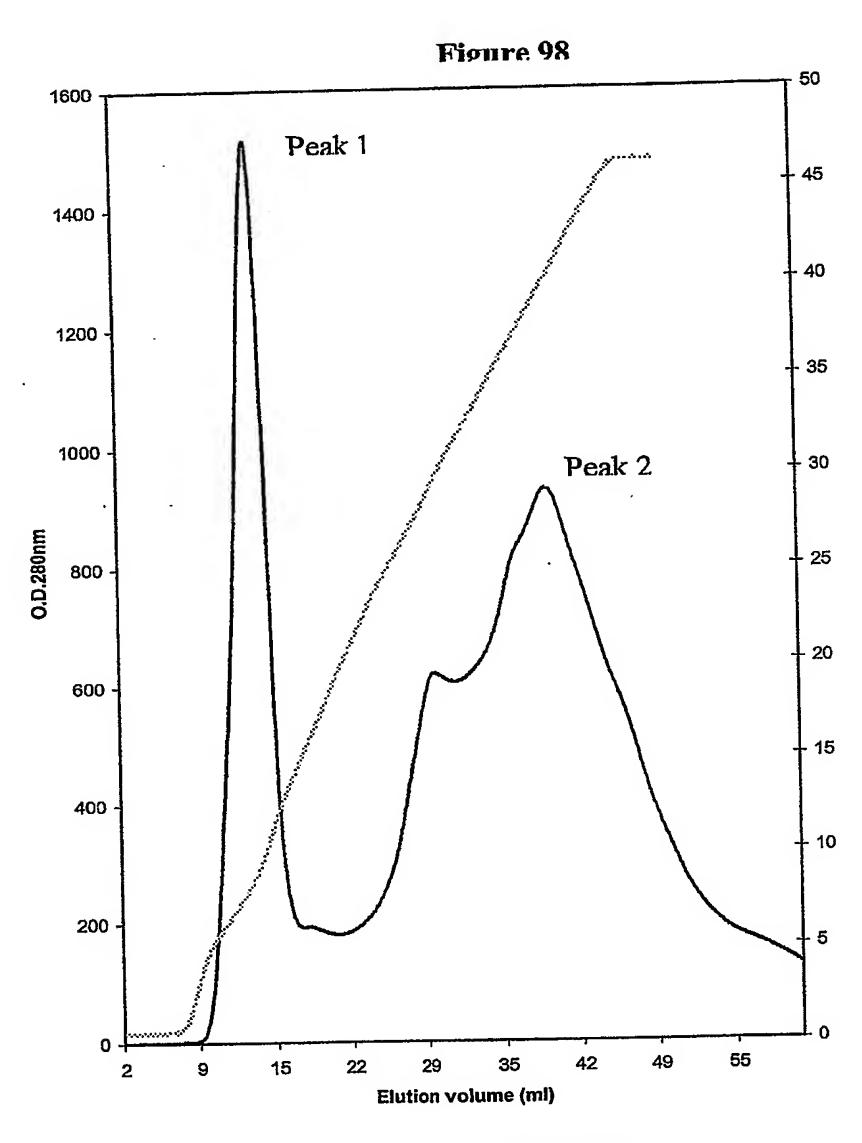
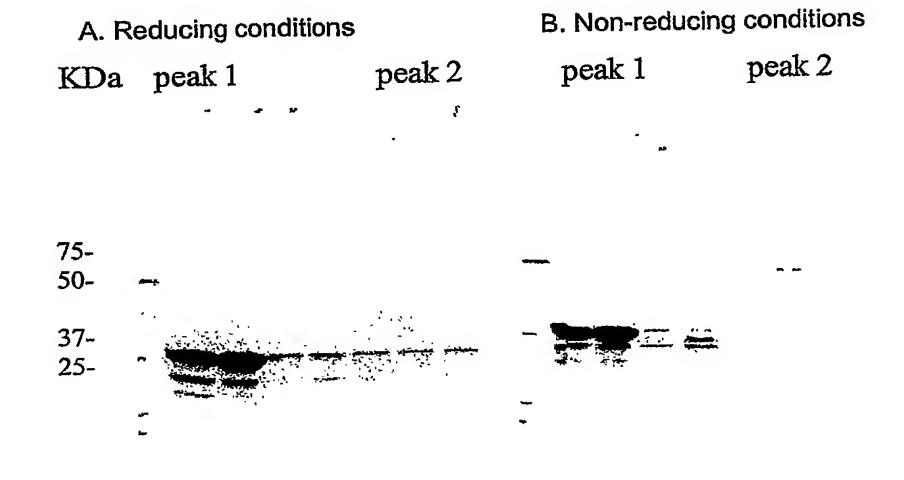
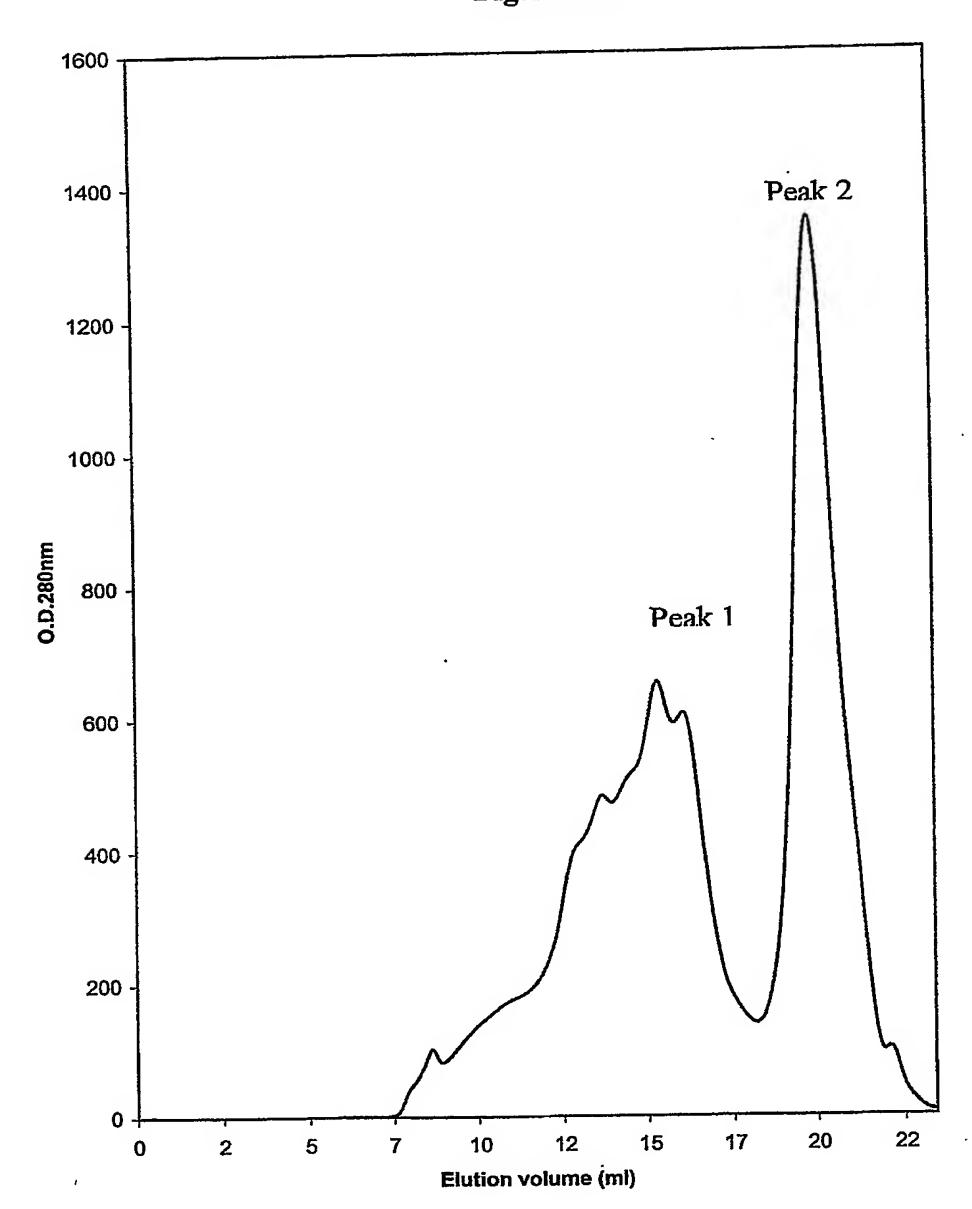


Figure 99



PCT/GB02/03986

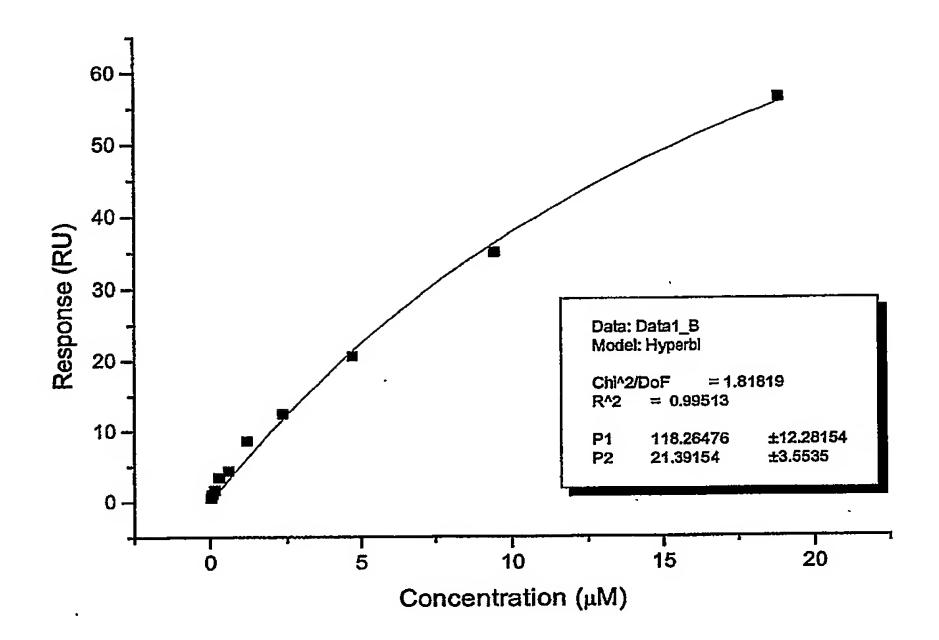
67/81 Figure 100



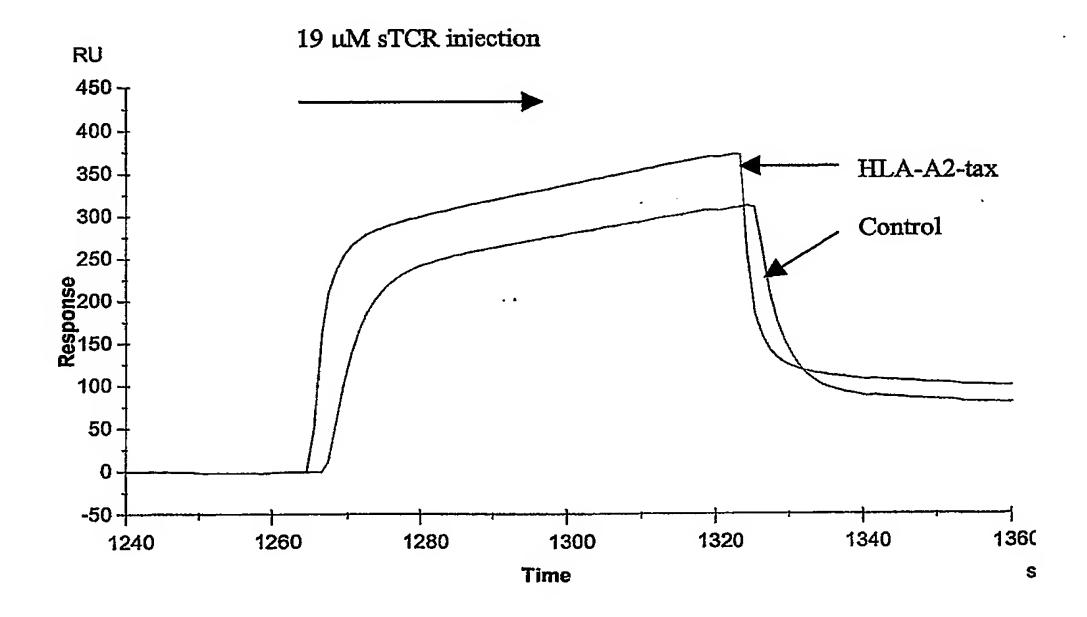
68/81 . Figure 101

 \mathbf{A}

WO 03/020763



 \mathbf{B}



69/81

Figure 102

70/81 Figure 103

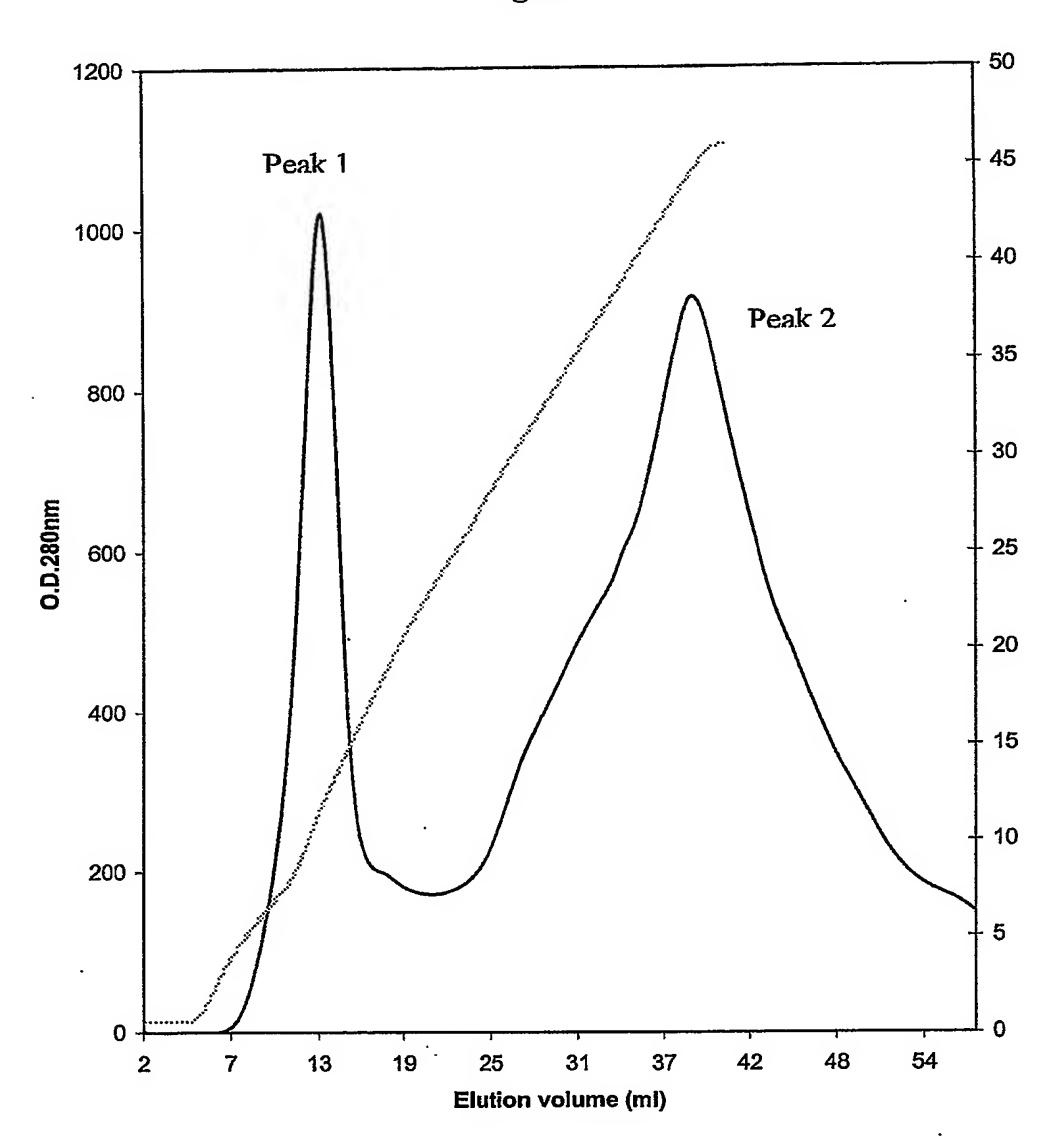
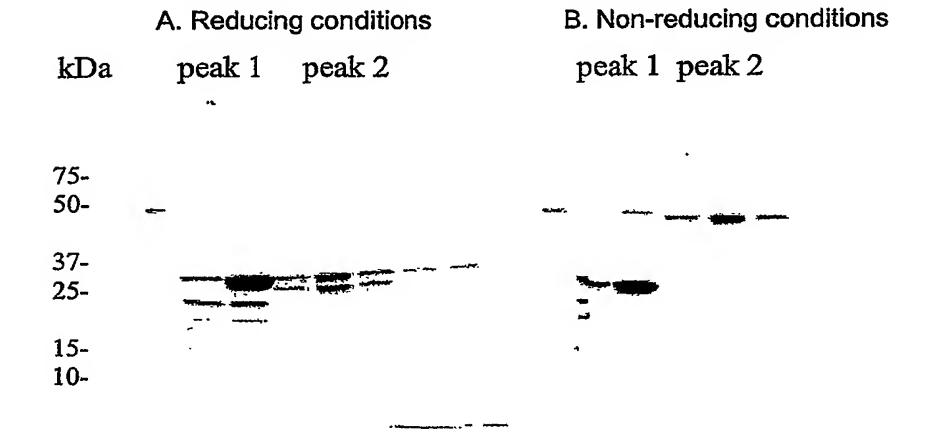
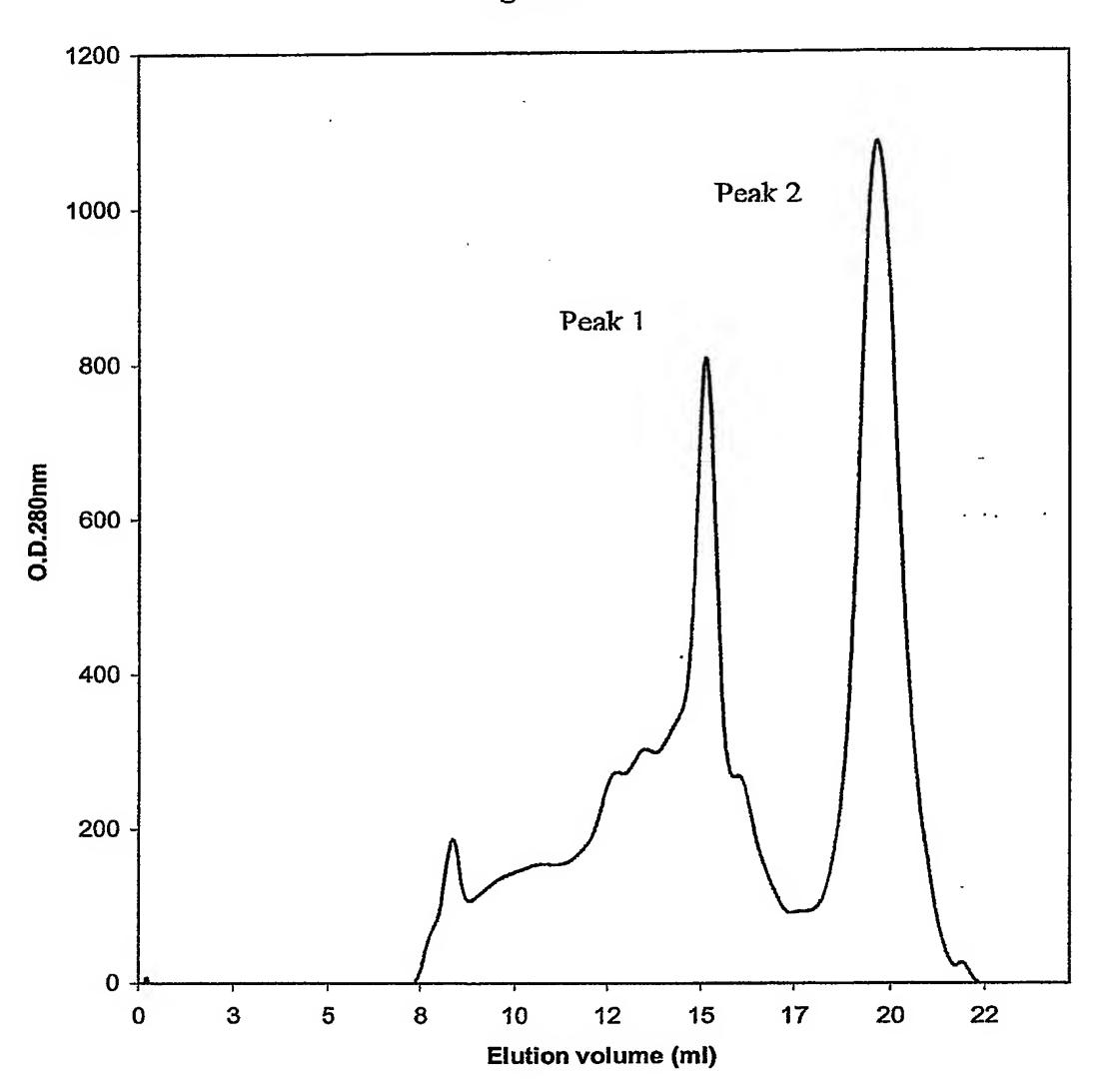


Figure 104

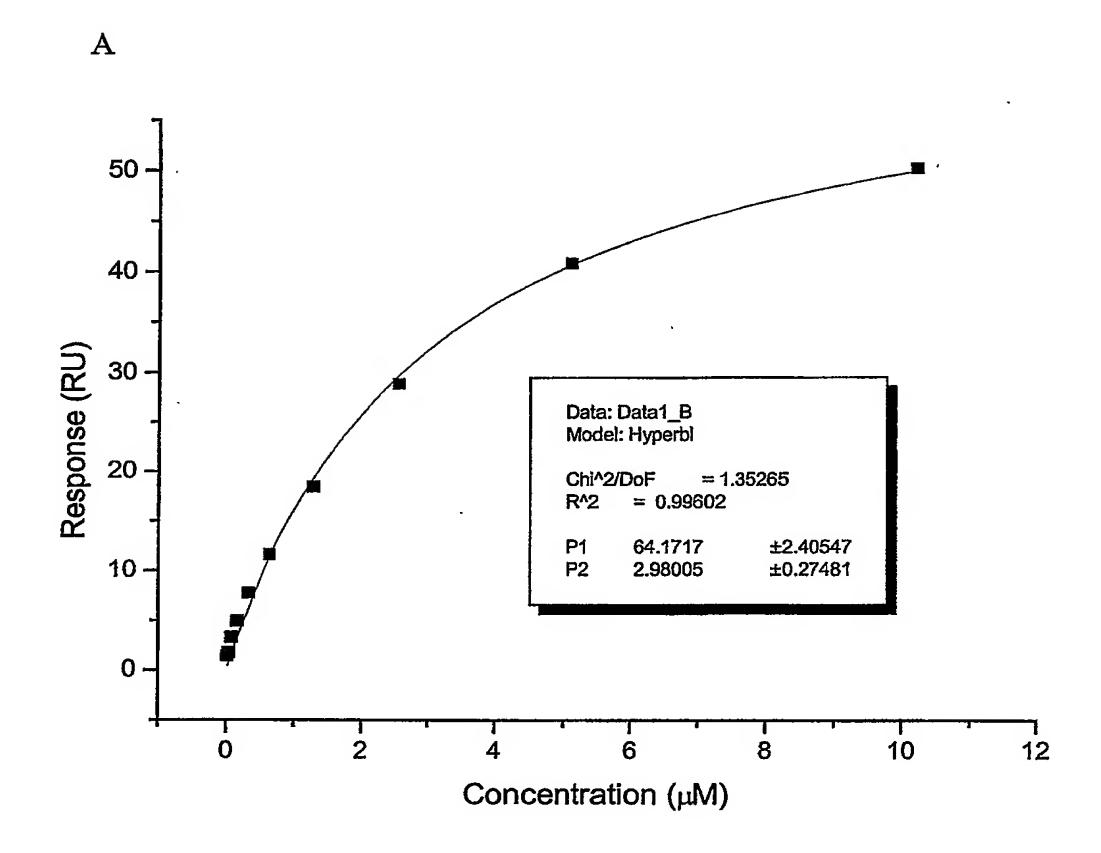


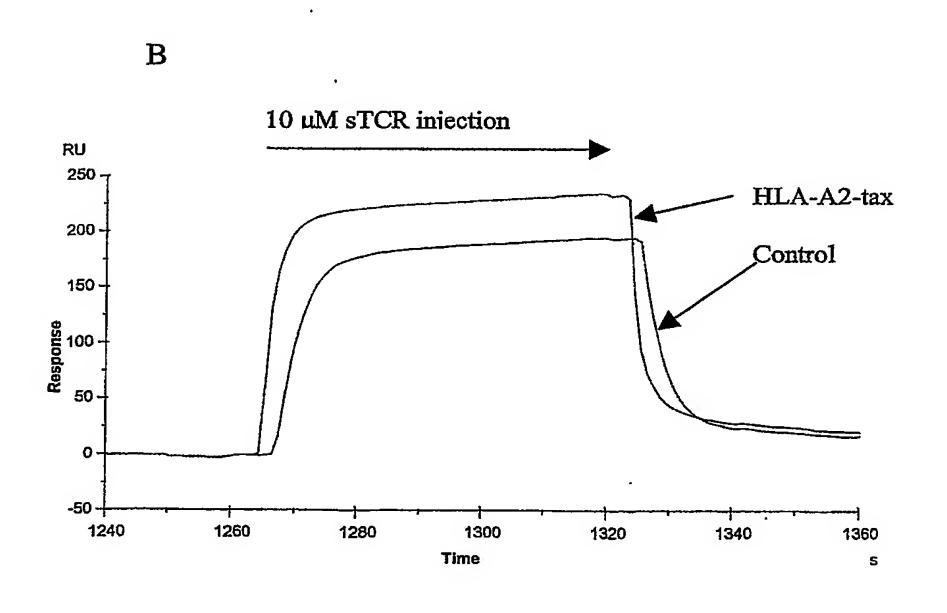
71/81 Figure 105



PCT/GB02/03986

72/81 Figure 106





AGCTAGCTAA AGCTCCAGCT CGCCTTGCAG GCGACGCGCT GACCCCAAAA GTGGACTCTT TGAGCTGATT CACACCGCAT GGCCGCATCT AATATTCTC GTTTGTTTCC GTTTGTTTCC GTTTGTTTCC GTTTGTTT
TCTCGAGCTC GTCTTTGTCT CCAACTTAAT GGCGAATGGC CTCCTTTCGC ACGGCACCTC TAGTTTTGCT TTCCAACAAT TGCGGCACCTC GACCACTTAA AAAAAAAAA AAAAAAAAAA
ACGCATGATA TITITITITITI CUTGGCGTTAC CAGCCTGAAT TAGGGGTTTTT AATGGAATAAA AATGTCAACG TAGGGCTTTTC AATGGAATAAA ACTGCAATTT AAAGAATAAA ACTGCAATTT AAAGAATAAA ACTGCAATTT AAAGAATAAA ACTGCAATTT AAAGAATAAA ACTGCAATTT AAAGAATAAA ACTGCAATG TTAAGAAAGGA TTTAATTTAGAAACTA ATGAAAAACTA ATGAAAAACTA ATGAAAAACTA ATGAAAAACTC AAGGGGATCT AGGGGATCT TTATGCAACTC AGACCACCGC CCTCCTTTTC ACGCGCACCC AAGGGGATCA TTATGCAACTC AGAGCAACTC TTATGCAACTC TTATGCAACTC CCTCCTTTCA AGACCACCC CCTCCTTTCA AGACCACCC CCTCCTTTCA AGACCAACTC CCTCCTTTCA AGACCACCC CCTCCTTTCA AGACCAACTC CCTCCTTTCA AGACCAACTC CCTCCTTCAACC CCTCCTTCAACC CCTCCTTCAACC CCTCCTTCTAACCC CCTCCTTCTAACCCC CCTCCTTCTAACCCC CCTCCTTCTAACCCC CCTCCTTCTAACCCC CCTCCTTCTAACCCC CCTCCTTCTAACCCCC CCTCCTCTTCAACCCC CCTCCTCTCTAACCCC CCTCCTCTCTAACCCC CCTCCCTC
GTGCCTGACT ATACATCCCT TGGGAAAACC AACAGTTCCGATT TTTGCCAGCGCC GGGTTCCCTTTCCC TGCCTCTTCCC TGCCTCTTCCC TGTCTCCCTTCC TGTCTCCCGAC TCCTTTTCCCC TGTCTCCCCC TGCCTCTTCCC TGTCTCCCCC TGTCTCCCCC TGTCTCCCCC TGTCTCCCCCC TGTCTCCCCC TGTCTCCCCC TGTCTCCCCC TGTCTCCCCC TCCTTTCCCC TCTTCCCCCCC TCTTCCCCCC
TCCGTATGAT TGACTGACG ACGTCGTGACC CGCCCTTCCCC CCGCTTCCCC TATAAGGGAT TAGCATCCTT AAAGAAACCG ATACTTCTTCTT TTTAGCGCT TAGCATCCTT TTTAGCGCT TAGCATCCTT TTTAGCGCT TAGCATCCTT TTTAGCGCT TAGCATCCTT TTTAGCGCT TTTAGCGCT TTTAGCGCT TTTTTGCCT TTTTTGCCT TTTTTGCCT TTTTTGCT TTTTTGCCT TTTTTTGCCC TTTTTTTGCCC TTTTTTTGCCC TTTTTTTT
CTAGTATTAA CTAGTATTAA CCGCACCGAT CCGCACCGAT TAAATCGGGG CTGATTAGT CCCCCAATGC GCCGATAACA AAAAAATTTC AAAAAAATTTC AAAAAAATTTC GCCCTATTAGT CCCCCTACCC GCCGATAACA TTTCAATTCC GCCGATAACA TTTCAATTCC GCCCCTAGA TTTCAATTCC GCCCTAGA TTTCAATTCC GCCCCTAGA TTTTAAATTTT TTTCAACACA CCCCCTAGA CCCCCTAGA CCCCCTAGA TTTTAAATTTA TCCCCCTAGA CCCCCTAGA CCCCCTAGA CCCCCTAGA TTTTAAATTTA TCCCCCTAGA CCCCCTAGA CCCCCTAGA CCCCCTAGA TTTTAAATTTA TCCCCCTAGA CCCCCTAGA TTTTAAATTTA TCCCCCCTAGA CCCCCTAGA TCCCCCCCCCC
TCTCTTGCCGTC TCTCTTGTTC TCACTGCCGC GCGAAGAGGC GGTGGTTACG GGTGGTTACG GGTGGTTACG CTCTAATTTG GGCCATCGCC TCTAAATTTG CTCTAATTTG GACAACGTC ACAACGTCAA TCTCTGTC ACAACGCC TGTAACTTCA TAATGCTTCA TAATGCTTCA TAATGCTTCA TAATGCTTCA TAATGCTTCA TAATGCTTCA TAATGCTTCA TCTTAAAAAA TACTTTAAAAAA TACTTTAAAAAA TACTTTAAAAAA TTGTTAAAAAA TTTTTCTAAAA TTGTTAAAAAA TTTTTCTAAAA TTGTTAAAAAA TTTTCTAAAAA TTGTTAAAAAA TTTTCTAAAAA TTTTCTAAAAA TTGTTAAAAAA TTTTTCTAAAAA TTTTTCTAAAAA TTGTTAAAAAA TTTTTCTAAAAA TTGTTAAAAAA TTTTTCTAAAAA TTTTTCTAAAAA TTTTTCTAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAA TTTTTCTAAAAA TTTTTCTAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTTAAAAAA TTTTTCTAAAAAA TTTTTCTAAAAAA TTTTTCTTAAAAAA TTTTTCTTAAAAAA TTTTTCTTAAAAAAAA
GGCCCACAGG GTTTTTCCTT TTAATTCATT TGGCGTGTGT CGGCGGGTGT CGGCGGTGT TCACGTAATA CGGCGGTGT TCACGTAGT TTTTAACAA TCACGTATT ATGACATT ATGACATT ATGACATT TTTGGGAATT TCCGCTTACG CACTCCTTACA GCTTCGGAGAT TCCGCTTTTTT ATGACAATT ATGACATT TTTGGGAATT TCCGCTTTTTA AGGTAAAAG AAGTAAAAAG AAGTAAAATT TTTGGGAATT TTTGGGAATT TTTGGGAATT TTTGGGAATT TTTGGGAATT TTTGGGAATT TTTGGGAATT TTTGGGAATT TTTGGGAATT ATTTGGGAATT TTTGGGAATT TTTGAACATTAAT TTCAACATTAAT TTCAACATTAAT TTCAACATAATA TTGAGCGTGGG GCCATACCAA GCCATACCAA GCCATACCAA GCCATACCAA GCCATACCAA TTTTAAAATA TTCAACATTAAT TTCAACATTAAT TTCAACATTAATA TTCAACATTAATA TTCAACATTAATA TTCAACATTAAAT TTCAACATTAAATA TTCAACATTAAATAATAATAATAATAATAATAATAATAAT
TGGATCCTAG AACAATGAAC TTAGTGAAC TTAGTGAGG TTTCGCCAGC GCATTAACGCGAA CTGATATTAAT GCATTCCCAGC GCGCACCCTC GCGACCCCCC GCGCACCCCC GCGCACCCCC GCGCCCCCCCC
CTGAATTCACCA CTGAATAAGG TTTGTTCCCT CACATCCCC CTGTAGCGGC TCCTTTTTA AACTTGTTTT TCTCAAATAT TCTCAAATAT TCTCAAATAT TCTCAAATAT TGCAGGTTTT TGCAAATGA TGCAAATGA TGCAAATGA TGCAAATGA TGCAAATGA TGCAAATGT TACGGAATGA ATCTTTTCT CTTCCTTCGT GGGCTTTTCC ATCTTTTCC ATCTTTTCC ATCTTTTCC AAAGTAAAAGG GAAATGTGGA AAAGTAAAAG GGGAACCGGA ACTTACTTTCCAAT TCAGAATGAC AAAGTAAAAG GGGAACCGGA ACTTACTCTA
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

Figure 107 continued

TGAGTTTTCG AAACCACCGC TCCTTCTAGT TGGCGATAAG TTGGAGCGAA	GCGGCAGGGT TCGATTTTTG	ATGTTCTTTC	CTGGAAAGCG GGAATTGTGA	CCGGCCGTCG	TAATTCTCTT	TTACCCGGCG	GAAGGCAAAA	TIGICICATG	CCATTATTAT	CCCTCATGGA	TAACGGGAGC	ACATAGTGTT	GAGGACCTCA	TCTAAGACTT AATTAAAGCA	TCGGCTGCTG	THALLCIAM
TCCCTTAACG GCAAACAAAA CCAAATACTG CTGCTGCCAG	TATCCGGTAA	TTTTGCTCAC	GGTTTCCCGA	GGGTACCGGG	AGGAACTGCA	CGAGITGCTC	GCAAAAACAG	ATCAGGGTTA	GTCTAAGAAA	TCTTCAGATT	CCAATGTTCC	AGACCTAACT	TTTAAACTGT	GATTACCCGT	_	ALTITICITI
ATGACCAAAA TCTGCTGCTT AGCGCAGATA TTACCAGTGG	GGCGGACAGG	TTTGCTGGCC	TGGCACGACA	AGGGCGAAT'I AAGGCGAGTT	TGGTTATGGC	ATGCGGCGAC	TTCTGGGTGA	TGAAGCATTT	GCCACCTGAC	TGGTCATTCT	GAATCGTTTA	ATTGTGAGGG	GTGAGCGGGA	GTTGGTGGAA		TTACGTAAAT. . G
TGATAATCTC CTGCGCGTAA GCTTCAGCAG GCTAATCCTG	AAGGGAGAAA TGTCGGGTTT	TTCCTGGCCT	TTAATGCAGC	GACTCACTAT	TTATCACTCA	AGAATAGTGT	TCACCAGCGT	TCAATATTAT	CCCGAAAGT	GATCTACGTA	CGAAGAGTTT	AAATGGACTG	CTACGTTAGT	AACCCATCAG	•	AACACATACA
AGATCCTTTT TCCTTTTTTTT AAGGTAACTG ACCTCGCTCT	ACGCTTCCCG	CTTTTTACGG GCTGATACCG	GGCCGATTCA	CTCGAAATAC AGCTCCGGTT	GGCCGCAGTG	AGTCATTCTG	TCTTTTACTT	TCTTCCTTTT		, -	GATGGACATA	CGTGCTACCC	TATAATAATC	TATATCTAGG	_	ACCTACAAAA
ATCTAGGTGA CTTCTTGAGA TCTTTTTCCG CCGCCTACAT	AGAAAGCGCC	GCAACGCGGC CTTTGAGTGA	CCCGCGCGTT	TTACGCCAAG		TACTCAACCA		ATACTCATAC	AGGGGTTCCG		AGAGACIIA AAATGGTTTA		TITITIGAGE	CCTTCGAGAT		TGAACTTGCA
ATTTAAAAGG ATCAAAGGAT AGCTACCAAC CTCTGTAGCA	GTGAGCTATG	• -		ATGACCATGA CGTTTGGTAT	_	GTGACTGGTG	_	GAAATGTTGA	ATAAACAAAT	ט נ	ATTCCTGATG		ATAATGCCAT	CTACTTATTC		AGGAGITIAG CITITICITGC
TTCATTTTA CGTAGAAAAG CCGGATCAAG ACTTCAAGAA				GGAAACAGCT	_	ATGCTTTTCT		GGGCGACACG	ATTTAGAAAA	•	ATTCCAGAGT	CGAATCCATC	Ξ.	CGGTATCACC		AGCATAATTI TGITIGIATT
GATTTAAAAC CGTCAGACCC GGTTTGTTTG TTAGGCCACC		CCCIGATICI		ATTTCACACA CATCGTGGTG	-	CATCCGTAAG		AAGGGAATAA	ATTIGAATGI	-	CATGGTATT	TGGAACTGGA	GGATATTTAA	ACACTICIGA TOTATTGATG		TATAAAGGGC TTCAATITTT
ACTTTAGATT TTCCACTGAG TACCAGCGGT GTAGCCGTAG	CGACCTACAC	TGATGCTCGT CTGCGTTATC	CGAGGAAGCG	GCGCATAACA	AAAAAAGCG	ACTGTCATGC	TGAGATCCAG	TGCCGCAAAA	AGCGATACAT	CATGACATTA	CCTAGTTACA	GTAATGGTGA	TAAAGATTAC	ATACATTCAG	ATCACACAAT	TAACAGGGAA
3801 3901 4001 4101 4201	4301 4401	4501 4601	4701 4801	4901 5001	5101	5201 5201	5401	5501	2601	~ C	5801 5901	6001	6101	6201	6401	6501 6601

AGCTAGCTAA AGCTCCAGCT CGCCTTGCAG GCGACGCCCC TTTCTTCCCT GACCCCAAA GTGGACTCTT TTGAACTAT TTGAACGCAC GCATCATCT TTGAACGCAC GCATCATCT TTGAACGCAC GCATCACTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCTTTT TCCCCCTTTT TCCCCCTTTT TCCCCTTTT TCCCCCTTTT TCCCCCTTTT TTTATATATTT TTTATATATTT TTTATATATTT CTTTTATATATT TTTATATATA
TCTCGAGCTC GTCTTTGTCT CCAACTTAAT GGCGAATGGC CTCCTTTAATA GGCGCACCTC TTCTTTAATA GGCGCACCTC TCCCTTTAATA GGAAATGCG CCCCAAGGCC CCCCAAGGCC AAAATTGCGG GAATTTATC TCGCTTCCC AAAATTGCGG CTCCTCCGGG CTCCTCCGGG CTCCTCCGGAACC TCGCTCCCGG GAATTTATC AAAATTGCGG AAAATTGCGG CTCCTCCGAAAA TCGATTTATAA CCCCCAACGCC AAAATTGCGG AAAATTGCGG AAAATTGCGG CTCCTTCCCG AAAATTGCGG AAAATTGCGG AAAATTGCGG AAAATTGCGG AAAATTGCGG AAAATTGCGG AAAATTGCGG AAAATTGCGG AAAATTGCGGAACCC AAAATTGCGAAATG ATCGATTTTTAA ATCGATTGAATG AACTTCGAATG AACTTCCCG AAGCTAATGG
TTTTTTTTTTT CTGGCGTTAC CTGGCGTTAC CTGGCCTTAT CTAGCGCCG TTAGCGTTT TATCGCCTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCCTTTCG TTGCGGAATCG TTTTTTACGGAAT GGGAAATGTG TGAAAGGAAT TGAAAGGA TCTCCAGAATG TGAAAGTAAA TGAAAGTAAA TGAAAGGAATGC TTGCGAAATGC TTGCGAAATGC TTGCCTTACTC
GTGCCTGACT ATACATCCCT TGGGAAAACC AACAGTTGCG TGCCACGCCC GGGTTCCGAT TTTGCCGATT TTTGCCGATT TTTGCCGATT TTTGCCGATC GTTCGAAGGA GCTTGACGTC TCGCCTCCC GCTTGACGT TCTGTCCATCC GTGCCTTCCC GTGCCTTCCC TCGCTTCCC TCGCCCCCC GTGCCCCCC GTGCCCCCC GTGCCCCCC TCGCCCCCC TCGCCCCCC TCGCCCCCC TCGCCCCCC TCCCCTTCCC TCCCCTCCC TCCCCTCCCC TCCCCCC
TCCGTATGAT TGACTGACCG ACGTCGTGAC GGCCTTTTA GCTCCCTTTTA GCTCCCTTTTA GCTCCCTTTTC GGCTTTTTCGC CTGATGCGC TATAAGGGGAT CTCTTTTTCGC CTCTTTTTCGC GCTTTTTCGC GCTTTTTTCGC CTCTTTTTCGC CTCTTTTTCGC CTCTTTTTCGC TATAATTCTGC GCTTTTTTCGC TATATGTGAGAG ACTCCTTTTTTCT GAAATGAAAAG ACTCTTTTTTTTCT TATAATTTTTTTCT GGCTTTTTTTTTCT TATATTTTTTTTCT GGCTTTTTTTTTCT TATATTTTTTTTTCT TATATTTTTTTT
CTAGTATTAA CTAGTATTAA CTAGTATTAA CCGCCCCGAT CCGCCCCCGAT TTACAATCGGGG CTATTACATTCC AACGTGGGGG CCATTCCATCC AACGTGGAGG CCATTCCATCC ACCCCCCCC ACCCCCCCCC CCAGTCGCTCC CCAGTCGCTCC ACCCCCCCCC ACCCCCCCCCA ACCCCCCCCCC
TCTCTTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
GGCCCAAAG GTTTTTCTTT TTAATTCAAT TGGCGTAATA CGGCGGTGT CGGCGGTGT CGGCGGTGT TTTTAACAAA AAAAAAAAA ATTGTTTTA AAAAAGCGTA TTTTAACGAGG ATTGTTTTA AAAAGCGTAC CTTGGTTTTA CCGGGAGCTG CTTGGTTTTA AAAAGCGTAC GAGTTTTTA AAAAGCGTAC GAGTTTTTA TTTTTTTTTT
TGGATCCTAG AACAATGAAC TTAGTGAAC TTTCGCCAGC GCATTAAGGG CCACGTTCGC GGGACAACAC GGGACCAACC GGGACCAACC GGGACCAACC GGGACCACC GTGATGATC GGGACCACC GTGATCAACC GTGATCAACC GTGATCAACC GTGATCAACC GTGATCATC GTGATC GTGAT
GRATTCACCA CTGAATAAGG TTTGTTCCCT CACATCCCCC CTGTAGCGGC TCGTAGCGGC TCTCTTCTCG AAAGGAGAAA TCTCACTTATGACT GAAAAAAA TCTTACTCTTA TTACTCTGT AAAGGCGCA TTTACTCTGT AAAGGCTTAAAA TCTTACTCTGT AGGTTTAAAA TGTTATAAAA TGTTATAAAA TGTTATAAAA TGTTATAAAA TGTTATAAAA TGTTATAAAA TGTTATAAAA TGTCACGGGC ATTCGTGTCGC GTGCCACGAGG ATTCGTGTCGC GTGCCACGAGG AAACGACGAGG AAACGACGAGG AAAACGACGGAGG AAAACGACGGAGG

Figure 108 continued

TT A	. 5	\$ 5	AG	AC	ଣ୍ଡ	ŢŢ	AT	AA	ည	iga i	AG) []		LLI	ATA	17G	ACA	FAA	Jer Jer	4GT	AGA	SCA SEA	1.1.A	TCA	CHC		GTA	
ACTTCATTTT		TGCCGGAICA	CCACTTCAAG	GACTCAAGAC	GATACCTACA	GAGGGAGCTT	CGGAGCCTAT	CTGTGGATAA	CCCAATACGC	ATTAATGTGA	CAGGAAACAG	TGTCACGCTC	TTCGGTCCTC	AGATGCTTTT	GCGCCACATA	AACCCACTCG	AAGGGCGACA	GTATTTAGAA	AAATAGGCGT	ATGACAGAGT	TTAT'ICCAGA	GACGAATCCA	AAC'I'TAC'I'IA	GACGGTATCA	TGTTACACTC	ATACCACCIC	GCAGCALAAL TTTGTTTGTA	
				_	<u> </u>	_	_	_	-	•	_	-	_			•	•	_	•	•	_	_	•	_	<u>-</u>			
TTGATTTAAA	いりなうさい	Greer rerr	AGTTAGGCCA	TACCGGGTTG	ACCGAACTGA	GAGAGCGCAC	GTCAGGGGG	TCCCCTGATT	CGGAAGAGCG	GCGCAACGCA	CAATTTCACA	GGCATCGTGG	CGGTTAGCTC	GCCATCCGTA	GGATAATACC	AGTTCGATGT	AAAAGGGAAT	ATATTTGAAT	TAACCTATAA	GCAGATGTAT	CACATGGTAT	GATGGAACTG	ACGGATATT	AGACACTICI	CCTCTATTGA	ATTCTCTCGG	AATATAAAGG TTTTCAATTT	
	•						_					_	-	_		•		_				·	•	•	_	·		
ATACTTTAGA		GCTACCAGCG	GTGTAGCCGT	AGICGIGICI	AACGACCTAC	GICGGAACAG	TGTGATGCTC	TCCTGCGTTA	AGCGAGGAAG	CGGGCAGTGA	GAGCGGATAA	CGAGCTTGAT	TGAAAAAAAG	TTACTGTCAT	CGTCAACACG	GTTGAGATCC	AATGCCGCAA	TGAGCGATAC	ATCATGACAT	GAGAAGIGCG	GICCIAGITA	GCGTAATGGT	TTTAAAGATT	CAATACATTC	TTTCAGCTT	CAATCACACA	TGTAACAGGG	
•		_	Τ.	•	. •	_	_	CTT			LIGI	CGI	STIE	CLC	CCGG	CGCT	3CAA	CICA	LATT	CATG	IGLL	GGGA	AGTG	ACCI	AGAC	AAAG	CHGC	-i) -i
TTACTCATAT	CGIGAGITI	AAAAACCACC	TGTCCTTCTA	AGTGGCGATA	GCTTGGAGCG	AAGCGGCAGG	CGICGAITIT	ACATGTTCTT	CGAGTCAGTG	GACTGGAAAG	GTGGAATTGT	GGCCGGCCGT	CCCCATGITG	CATAATICIC	TCTTGCCCGG	TCTTACCGCT	AGGAAGGCAA	TATTGTCTCA	AACCATTATT	TICCCICAIG	AGATGTTGTT	CCTAACGGGA	CTACATAGTG	GIGAGGACCI	GTTCTAAGAC	TTAATTAAAG	GCTCGGCTGC TTTTT ATTTT	47674 7 7 7 7
		Ĭ			_				_		_	_									CCAG	TGTT	CTAA	AACT	ACCC	GAAA	TTTE	-1
CAGACCAAGT	AATCCCTTAA	TTGCAAACAA	TACCAAATAC	GGCIGCIGCC	ACACAGCCCA	GGTATCCGGT	CTGACTTGAG	CCTTTTGCTC	CCGAGCGCAG	CAGGTTTCCC	CCTAIGITGI	TIGGGTACCG	TTACATGATC	GCAGGAACTG	ACCGAGITGC	CICICAAGGA	GAGCAAAAAC	TTATCAGGGT	ACGTCTAAGA	CTTCTTCAGA	GAAGACCCAG	TACCAATGTT	GGAGACCTAA	GATTTAAACT	AAGATTACCC	TTCTCCGAAA	TATACCITIG	rituru
CTGT	CCAA	CIGC	CAGA	CAGT	GTGC	GACA	ACCT	CTGG	ACGA	ACGA	GGCT	SCGAA	SCGAG	TATG	SEGCE	FAAAA	IGGGT	AGCAT	ACCTG	CATT	AGAGA	CGTT	STGAG	AGCGG	GGTGG	rgaga	GCCTA	ed the
TGGTAACTGT	TCA'I'GACCAA	AATCTGCTGC	AGAGCGCAGA	TGTTACCAGT	GGGTTCGTGC	AAGGCGGACA	TTCGCCACCT	CTTTTGCTGG	AGCCGAACGA	GCTGGCACGA	GCTTCCGGCT	ATAGGGCGAA	TCAAGGCGAG	CATGGTTATG	GTATGCGGCG	GGGCGAAAA	GTTTCTGGGT	ATTGAAGCAT	GTGCCACCTG	TATGGTCATT	AGGCAAGAGA	TTGAATCGTT	TGATTGTGAG	GTGTGAGCGG	AGGITGGIGG	GCATGTGAGA	AAGGAGCCTA	CAG
							_		_			·							_	<u>-</u>	_ •	_	Ī.,	Τ.		_	TGCA .	CATA
GATTAAGCAT	TTTGATAATC	TTCTGCGCGT	IGGCTICAGC	CTGCTAATCC	GCTGAACGGG	CGAAGGGAGA	CCTGTCGGGT	GGTTCCTGGC	CGCTCGCCGC	CATTAATGCA	TACACTTŸAT	ACGACTCACT	TTCCCAACGA	TGTTATCACT	TGAGAATAGT	AACGTTCTTC	TTTCACCAGC	TTTCAATATT	TCCCCGAAAA	GGGATCTACG	CTTCCATGAT	TACGAAGAGT	CCAAATGGAC	TCCTACGTTA	GGAACCCATC	ATCTTCAGTG	TGCTAATGCA	IAITIICCU AAAACACATA
	_	_					_						_		_			_				٠,		Ξ.	<u> </u>			
GIGCCICACI	GAAGATCCTT	GATCCTTTTT	CGAAGGTAAC	ATACCTCGCT	CAGCGGTCGG	CCACGCTTCC	TCTTTATAGE	GCCTTTTAC	GAGCTGATAC	TIGGCCGATT	CCCCAGGCTT	AGCTCGAAAT	TCAGCTCCGG	TTGGCCGCAG	CAAGTCATTC	ATCATTGGAA	CATCTTTAC	ACTCTTCCTT	CGCGCACATT	TCAAGAATTG	TATTCAGGCA	TAGATGGACA	ACCGTGCTAC	GTTATAATAA	ATTATATCTA	CCAGITITIA	TTGTTACGCA	CAACAITIAC ATAACTACAA
																				_				_				
GCTGAGATAG	GGATCTAGGT	ATCTTCTTGA	ACTCTTTTTC	CACCCCCTAC	GGATAAGGCG	TGAGAAAGCG	ACGCCTGGTA	CAGCAACGCG	GCCTTTGAGT	TCCCCGCGCG	TCATTAGGCA	GATTACGCCA	ATGGCTTCAT	CAGAAGTAAG	TGTACTCAAC	AAAAGTGCTC	TGATCTTCAG	GAATACTCAT	ATAGGGGTTC	CCTTTCGTCT	CAAGAGACTT	TGAAATGGTT	CGTCCTGAGG	ATTTTTGA	TCCCTTCGAG	TTTCTGGCAT	GACAGGTGGT	AGTGAACTTG GCTTAAATCT
_													-	_					_								_	
TAGACAGATC	TAATTTAAAA	AGATCAAAGG	AGAGCTACCA	AACTCTGTAG	GATAGTTACC	GCGTGAGCTA	CCAGGGGAA	GGAAAAACGC	CCGTATTACC	AAACCGCCTC	GTTACCTCAC	CTATGACCAT	GICGILIGGI	CGATCGTTGT	CTGTGACTGG	GCAGAACTTT	TGCACCCAAC	CGGAAATGTT	AAATAAACAA	ATCACGAGGC	CGCCAGITIC	GTATTCCTGA	TCAATAGATA	GAATAATGCC	CCCTACTTAT	GGACACCCCT	GGTTGAAACT	TTCTTTTCTT TTCTTTTCTT
TAGA	TAAT	AGAT	AGAG	AACT	GATA	GCGT	CCAG	GGAA	CCGT	AAAC	GTTA	CTAT	GICG	CGAI	CIGI	GCAG	TGCA	CGGA	AAAT	ATCA	CGCC	GTAI	TCAZ	GAAT	CCCI	GGAC	GGTJ	TTCI
380I	3901	4001	4101	4201	4301	4401	4501	4603	4703	4801	4901	5001	5101	5201	5301	5401	5501	60	5701	5801	5901	6001	6101	6201	6301	6401	6501	6601 6701

AspPheAspSer GlyLysGlyLeu GluThrAlaGln GlyArgSerThr LeuTyrIle PhelysSerAsn SerAlaVal ThrasnasnGly LeuLeuPhe TICTICCCCA GCCCAGAAAG TICCTAACTC CTACCTCTGT GCTGTGAGGC CCACATCAGG AGGAAGCTAC ATACCTACAT TTGGAAGAGG AACCAGCCTT GICIAIGGAC ITCAAGAGCA ACAGIGCIGI CCTATICACC GAITITGAIT TAAATCATCA GGACGTAGTA CTTTATACAT ThrSerLeu Valserieu Asplysarg Glualaglu Alagingluval ThrGinile ProAlaAla Grand Argentian Alagingluval ThrGinile ProAlaAla GGGAAAGGTC PheAsnAsnSer IleIlePro GluAspThr PhePheProSer ProGluSer Ser*** GlyArgGly LeuPheThr GCAGGACCCT GlnAspPro and cerebral manufacture of the content of the cont IleProThrPhe SerSerAspLys SerValCys Tyrasnleugln TrpPhearg TCCAGTGACA AGTCTGTCTG SerMetAsp TAGCGCTAIT TACAACCICC AGIGGITIAG GlnserSerGln ArgGluGln ThrSerGly ArgLeuAsnAla SerLeuAsp LysSerSer AspValAlaVal LeuProPhe SerAsnSer LysCysValleu AspMetArg AlaAlaProVal GGCCTGGAGC AACAATCTG ACTTTGCATG TGCAAACGCC TTCAACAACA GCATTATTCC AGAAGACACC AGACTTAATG CCTCGCTGGA GlnProGlyAsp SerAlaThr TyrLeuCys AlaValArgPro ThrSerGly GlySerTyr Serlysaspser aspvaltyr ilethrasp Lyscysvalleu AspMetarg Agtaaggatt crgargrgra tarcacagac aaatgrgrgc tagacargag IleValHisPro TyrIleGln AsnProAsp ProAlaValTyr GinLeuArg AspSerLys AGACTCTAAA LeuSerValPro GluGlyGlu AsnLeuVal LeuAsnCysSer PheThrAsp SerAlalle SerAlaLeu ATTGITCATC CGIATATCCA GAACCCGGAT CCTGCCGTGT ACCAGCTGAG TCACATCTCT GTTGCTTATT CAGTCAAGTC AGAGAGAGCA AACAAGTGGA CIGAGIGICC CAGAAGGAGA AAACIIGGIT CICAACIGCA GITICACIGA yAspPhe MetArg PheProSer IlePheThr AlaValleuPhe Aloratrong Caattrong Canthology Caattrong Canthology Caattrong Caa CTCAAACAAA TGTGTCACAA AGTAAGGATT CTGATGTGTA TAT ·AlaTrpSer AsnLysSerAsp PheAlaCys AlaAsnAla TGCAGCTTCT CAGCCTGGTG ACTCAGCCAC ··ThrSerLeu LeuLeulle ..GlnThrAsn ValSerGln .AlaAlaSer 401 601 801 901 201 501 701 101 301 H

The pre-pro mating factor alpha sequence is highlighted. BamHI site is underlined.

The pre-pro mating factor alpha sequence is highlighted.

Figure 111

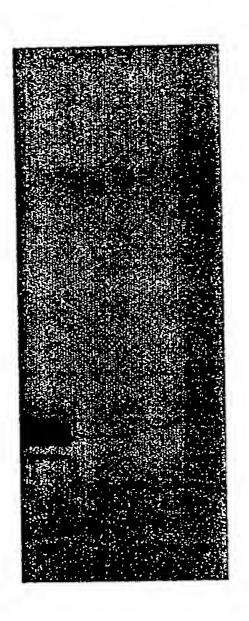


Figure 112

ggatccagcatggtgtgtctgaagctccctggaggctcctgcatgacagcgctgaca gtgacactgatggtgctgagctccccactggctttgtccggagacaccggtggcgga tctctagttccacgcggtagtggaggcggtggttccggagacacgcgttagtaggtc gacggaggcggtggggtagaatcgcccggctggaggaaaaagtgaaaaccttgaaa gctcagaactcggagctggcgtccacggccaacatgctcagggaacaggtggcacag cttaaacagaaagtcatgaactactaggatcc

Figure 113

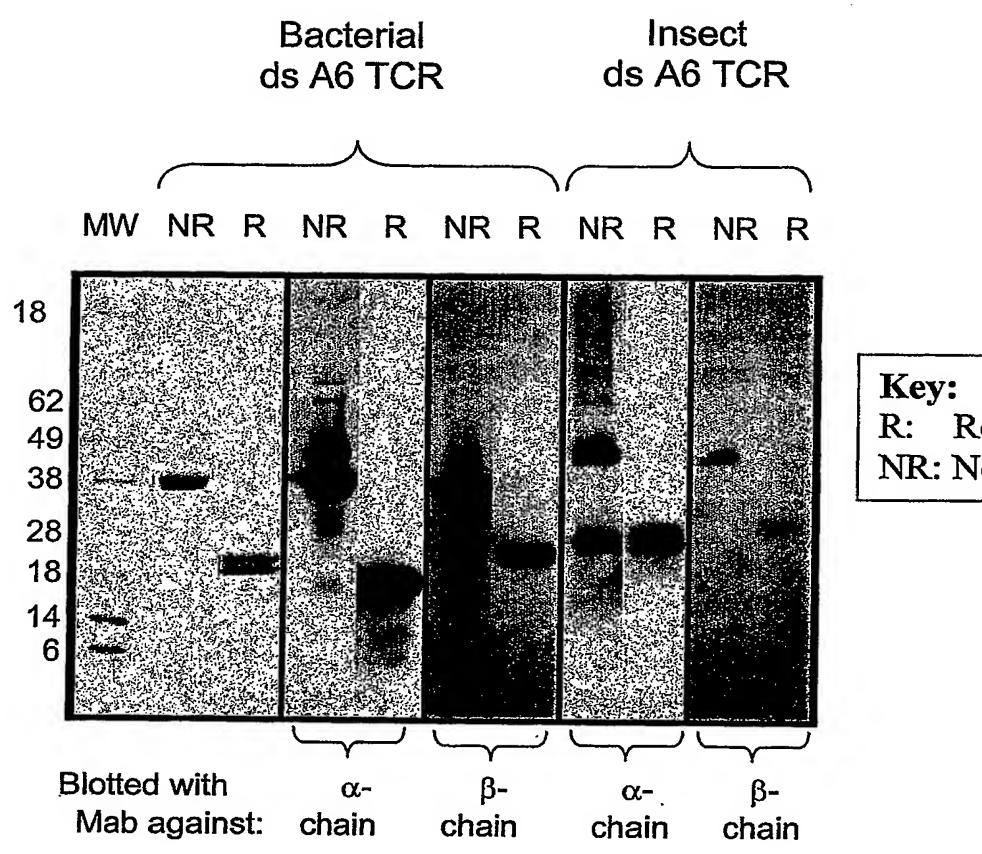
BamHI	•	AgeI		Sal	II	BamHI
	DRβ Leader —	GDT	TCR chain	Stop	Zipper	

ggatccagcatggtgtctgaagctccctggaggctcctgcatgacagcgctgaca gtgacactgatggtgctgagctccccactggctttgtccggagacaccggagacacc ggacagaaggaagtggagcagaactctggacccctcagtgttccagagggagccatt gcctctctcaactgcacttacagtgaccgaggttcccagtccttcttctggtacaga caatattctgggaaaagccctgagttgataatgtccatatactccaatggtgacaaa atcagagactcccagcccagtgattcagccacctacctctgtgccgttacaactgac agctgggggaaattgcagtttggagcagggacccaggttgtggtcaccccagatatc cagaaccctgaccctgccgtgtaccagctgagagactctaaatccagtgacaagtct gtctgcctattcaccgattttgattctcaaacaaatgtgtcacaaagtaaggattct gatgtgtatatcacagacaaatgtgtgctagacatgaggtctatggacttcaagagc aacagtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaac aacagcattattccagaagacaccttcttccccagcccagaaagttcctaagtcgac ggaggcggtggggtagaatcgcccggctggaggaaaaagtgaaaaccttgaaagct cagaactcggagctggcgtccacggccaacatgctcagggaacaggtggcacagctt aaacagaaagtcatgaactactaggatcc

Figure 115

ggatccagcatggtgtctgaagctccctggaggctcctgcatgacagcgctgaca gtgacactgatggtgctgagctccccactggctttgtccggagacaccggagacacc ggaaacgctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagc atgacactgcagtgtgcccaggatatgaaccatgaatacatgtcctggtatcgacaa gacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgac caaggagaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccg ctcaggctgctgctgctccctcccagacatctgtgtacttctgtgccagcagg ccgggactagcgggggggccaccagagcagtacttcgggccgggcaccaggctcacg gtcacagaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatca gaagcagagatctcccacacccaaaaggccacactggtgtgcctggccacaggcttc taccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtggg gtctgcacagacccgcagccctcaaggagcagcccgcctcaatgactccagatac gctctgagcagccgcctgagggtctcggccaccttctggcaggacccccgcaaccac ttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccaggat agggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagactaa gtcgacggaggcggtgggggtagaatcgcccggctggaggaaaaagtgaaaaccttg aaagctcagaactcggagctggcgtccacggccaacatgctcagggaacaggtggca cagcttaaacagaaagtcatgaactactaggatcc

Figure 116



R: Reduced

NR: Non-reduced